



## SEQUENCE LISTING

<110> Yacoby-Zeevi, Oron  
<120> METHODS OF AND PHARMACEUTICAL COMPOSITIONS FOR IMPROVING  
IMPLANTATION OF EMBRYOS  
<130> 01/22716  
<140> US 09/979,297  
<141> 2001-10-17  
<150> US 09/260,037  
<151> 1999-03-02  
<150> US 09/140,888  
<151> 1998-08-27  
<150> US 09/046,475  
<151> 1998-03-25  
<150> US 08/922,170  
<151> 1997-09-02  
<150> PCT/US 60/240,037  
<151> 2000-10-17  
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<170> PatentIn version 3.3  
<210> 1  
<211> 543  
<212> PRT  
<213> Homo sapiens  
<400> 1

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu  
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Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
 165 170 175  
 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
 180 185 190  
 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
 195 200 205  
 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
 210 215 220  
 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
 225 230 235 240  
 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
 245 250 255  
 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
 260 265 270  
 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
 275 280 285  
 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
 290 295 300  
 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
 305 310 315 320  
 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
 325 330 335  
 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala  
 340 345 350  
 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys  
 355 360 365  
 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val  
 370 375 380  
 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
 385 390 395 400  
 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
 405 410 415  
 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
 420 425 430  
 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
 435 440 445  
 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
 450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
500 505 510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
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Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
530 535 540

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atagcagct gacctga

17

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<220>  
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24

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<212> DNA  
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<220>  
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ctgtccaact caatggtcta actc

24

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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide

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<210> 6  
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<212> DNA  
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60

agatgctgct gcgctcgaag cctgcgctgc cgccgcgct gatgctgctg ctctggggc

120

cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg 180  
 acctggactt cttcaccag gagccgctgc acctgggtgag cccctcggtc ctgtccgtca 240  
 ccattgacgc caacctggcc acggaccgc ggttcctcat cctcctgggt tctccaaagc 300  
 ttcgtacctt ggccagaggc ttgtctctg cgtacctgag gtttggtggc accaagacag 360  
 attcctaata tttcgatccc aagaaggaat caacctttga agagagaagt tactggcaat 420  
 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt 480  
 tacggttggg atggccctac caggagcaat tgctactccg agaactactac cagaaaaagt 540  
 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct 600  
 caggactgga cttgatcttt ggctaaatg cgttattaag aacagcagat ttgcagtgga 660  
 acagttctaa tgctcagttg ctctgggact actgctcttc caaggggtat aacatttctt 720  
 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt 780  
 cgcagttagg agaagattwt attcaattgc ataaacttct aagaaagtcc accttcaaaa 840  
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 tcaccaagta cttgcggtta ccctatcctt tttctaacia gcaagtggat aaataccttc 1500  
 taagaccttt gggacctcat ggattacttt ccaaactctg ccaactcaat ggtctaactc 1560  
 taaagatggt ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa 1620  
 gttcactggg cttgccagct ttctcatata gttttttgt gataagaaat gccaaagttg 1680  
 ctgcttgcac ctgaaaaata aatatactag tcctgacact g 1721

<210> 7  
 <211> 543  
 <212> PRT  
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<220>  
 <221> misc\_feature  
 <222> (246)..(246)  
 <223> Tyr or Phe

<400> 7

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu  
 1 5 10 15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
 20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
 35 40 45  
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
 50 55 60  
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
 65 70 75 80  
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
 85 90 95  
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
 100 105 110  
 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
 115 120 125  
 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
 130 135 140  
 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
 145 150 155 160  
 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
 165 170 175  
 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
 180 185 190  
 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
 195 200 205  
 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
 210 215 220  
 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
 225 230 235 240  
 Gln Leu Gly Glu Asp Xaa Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
 245 250 255  
 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
 260 265 270  
 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
 275 280 285  
 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
 290 295 300  
 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
 305 310 315 320  
 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
 325 330 335  
 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala

[illegible]